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RESULT 11 G15289/c

KEYWORDS SOURCE ORGANISM

AUTHORS JOURNAL COMMENT REFERENCE

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Baldwin, J. Barna, N. Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P. Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funce, R., Gage, D., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McEwald, M., Macdonald, P., Marquis, N., Mocrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., StangerThomann, N., Stojanovic, N., Santos, R., Savery, P., Tesfaye, S., Titrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997)

http://ftp.genome.washIngton.edu/RW/RepeatMasker.html.

* NOTE: This record contains 70 individual

* Sequencing reads that have not been assembled into and the order in which they appear is completely

* arbitrary. Low-pass Sequence sampling is useful for overlap relationships among clones to be deduced.

* Overlap relationships among clones to be deduced.

* Will be sequenced to completion. In the event that

* Will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                        ACU12422 53967 bp DNA HTG 27-OCT-1999
HOMO Saptens chromosome 15 clone 141_E_4 map 15, LOW-PASS SEQUENCE
AC012422
                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 53967)
1 Lases, Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone 141_E.4
                                                     Length 250;
                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     722: contig of 722 bp in length
gap of unknown length
1504: contig of 782 bp in length
gap of unknown length
2265: contig of 761 bp in length
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3025: contig of 760 bp in length
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of 766 bp in length
unknown length
                                  Ouery Match
Best Local Similarity 100.0%; Pred. No. 4e-43;
Matches 98; Conservative 0; Mismatches 0;
                                                                                                                                                                     gap of
3791: contig
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HTG; HTGS_PHASE0.
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KEYWORDS
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Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
7753
                 04-JAN-1996
                                                                Prepared with primer pairs derived from T65388--Merck/UniEST.
                                                                                                                                 94 degrees C for 15 seconds
62 degrees C for 23 seconds
72 degrees C for 30 seconds
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanford niversity School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 others
                                                                                                                                                                                                                                                                               SIS
                                                                                                                                                                                                                                                                                                                               STS sequence: primer; sequence tagged site. human.
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each 1 um
each 200 um
0.05 units/ul
10 ul
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Stanford Human Genome Center (SHGC)
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Primer B: GGACGGACCAGCATCTGG
STS size: 131
PCR Profile:
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/organism-"Homo sapiens"
67. .197
67. .88
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Email: myers@shgc.stanford.edu
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50 mM
20 mM
8.3
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48 c 43 g
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Annealing:
Polymerization:
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Thermal Cycler;
                                                                                                                                                                                                                                                               human STS SHGC-15950.
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Total Vol;
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dNTPs:
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Tris-HCl:
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primer_bind
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unknown length of 817 bp in length

gap of contig contig of contig

4608:

3792

Source

FEATURES

BASE COUNT

unknown length

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Location/Qualifiers
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58 c 3
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Best Local Similarity 99.44;
Matches 171; Conservative
                                                                                                                                                                     sequence tagged site.
G43056
G43056.1 G1:4191973
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Gelatin:
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G43056
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/db_xref="61:4572462"
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/franslation="MGSVSELISGHSFRR"
/franslation="MGSVSELISGHSFRRR"
/franslation="MGSVSELISGHSFRR"
/franslation="MG
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Ishil, H., Baffa, R., Numata, S.I., Murakuno, Y., Rattan, S., Inoue, H., Mori, M., Fidanza, V., Aldar, H. and Croce, C.M.
The FE21 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 231)
National Pattan, S., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,
Mori, M., Fidanza, V., Alder, H. and Croce, C.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                             AF123652 231 bp mRNA PRI 07-APR-1999
Homo sapiens clone E16T8 FEZ1 (FEZ1) mRNA, alternatively spliced,
complete cds.
                                                           112 tegcagtacaagetgegcaagteeteecaceteaagaageteaaceggtatteegaeggg 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCGCAGTACAAGCTGCGCAAGTCCTCCCACCTCAAGAAGCTCAACCGGTATTCCGACGGG 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 TAGGCTTANACCTGGNATCTACAAGACCAAAAGTCCCTCCCTGCCTGAGGGCAGTACCCTC 60
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                                                                                                                                                                              1.8%; Score 162; DB 40; Length 231;
100.0%; Pred. No. 6e-79;
.lve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone-"E16T8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dene-"FE21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 162; Conservative
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JOURNAL

FEATURES

CDS

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REFERENCE AUTHORS

JOURNAL

TITLE

RESULT AF123652 LOCUS

ACCESSION

ö 1. .172
/organism="Homo sapiens"
/db_xref="texon:9606"
/map="42.70 cR from top of Chr8 linkage group"
/clone_lib="Human THudson SANGER"
/note="human STS created from EST in the Sanger database" custom built by IAS, Costar, Cambridge MA Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherid; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 172)

1 (bases 1 to 172)

1 (bases 2 to 172)

2 (bandour, Ean, J. B., Siao, C. J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Perkins, N., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Hale, L., Topaloglou, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and Gaps G43056 172 bp DNA STS 27-JAN-1999 WIAF-1517-STS Human THudson SANGER Homo sapiens STS genomic, 94 degrees C for 4.00 minutes 94 degrees C for 50.0 seconds 58 degrees C for 1.50 minutes 72 degrees C for 1.00 minutes 30 ö Large-scale identification, mapping, and genotyping of single-pucleotide polymorphisms in the human genome Science 280 (5366), 1077-1082 (1998) Length 172: Whitehead Institute/AIT Center for Genome Research Whitehead Institute/AIT Center for Blomedical Research Whitehead Institute for Blomedical Research Cambridge Center, Cambridge MA 02142 USA 7 252 1900 Indels Score 121; DB 13; Pred. No. 5.3e-56; 0; Mismatches 1; u 10 ng each 5 pM 4 nM 0.5 U Email: thudson@genome.wi.mit.edu Primer A: TAGGCTTAAACCTGGAATCTAC Primer B: CTCACTGGGAGGAAAAC STS Size: 172

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itle:
erfect score:
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Gapop 60.0 , Gapext 60.0
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9048
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                          em_ba2: •
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em_hum4: •
                                                                                                                          gb_htg2:*
gb_in1:*
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-5616.025 Million cell updates/sec
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   AF123653
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AF123653 9108 bp I
Homo sapiens FZZI (FEZI)
AF123653
AF123653.1 GI:4572463
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Match
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AF123656
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                                                                                                   ALIGNMENTS
                        gene, complete
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AC0011371 Homo sapi
AL03569 Homo sapi
AL035549 Homo sapi
AL001573 Homo sapien
AL00149547 Homo sapien
AL121601 Homo sapien
AL121601 Homo sapi
AL00933 Homo sapi
AC007097 Homo sapi
AC013612 Homo sapi
AC016157 Homo sapi
AC011857 Homo sapi
                                                                                                                                 AC006021 Homo sapi.
AL121971 Homo sapien
295152 Homo sapien
AC006538 Homo sapi.
AC007375 Homo sapi.
AC003682 Homo sapi.
AC008569 Homo sapi.
AC009280 Homo sapi.
AL121885 Homo sapi.
AC006966 Homo sapi.
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G60003 SHGC-130794

AF123652 Homo sapt

G43056 WIAF-1517-S

G15289 human STS

G15289 human sapt

AC011963 Homo sapt
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AF123659 Homo sap
AF123656 Homo sap
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AF123654 Homo
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AF123657 Homo
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Protocol:
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primer_bind
BASE COUNT
                                                                                                                                         human.
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                       RESULT
G43056
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/product=FE21*
/protein_id="AbD23833.1"
/db_xref="G1:4572462"
/db_xref="G1:4572462"
/translation="MGSVSSIJSGHSFHSKHCRASQYKLRKSSHLKKLNRYSDGLLRF
/translation="MGSVSSIJSGHSFHSKHCRASQYKLRKSSHLKKLNRYSDGLLRF
GFSQDSGHGKAMTRCPRASSMSGSCGRRRRRR"
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                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Hetazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutherla; Primaces; Catarrhini; Hominidae; Homo.

[ bases 1 to 231)
Ishii.H., Baffa.R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H., Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FE21 gene at chromosome 8p22 encodes a leucine-zipper protein, and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 231)
Ishli,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Ishli,H., Baffa,R., Alder,H. and Croce,C.M.
Divot, M., Fidanza,V., Alder,H. and Croce,C.M.
Divect Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
Location/Qualifiers
                                                                                                                                                                AF123652 231 bp mRNA PRI 07-APR-1999
Homo sapiens clone E16TB FE21 (FE21) mRNA, alternatively spliced,
complete cds.
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                                                                                     Ouery Match
1.8%; Score 162; DB 40; Length 231;
Best Local Similarity 100.0%; Pred. No. 6e-79;
Matches 162; Conservative 0; Mismatches 0; Indels
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome-"8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone-"E16T8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"FE21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .231
/gene="FEZ1"
                                                                                                                                                                                                                                                    AF123652.1 GI:4572461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermal Cycler: custom built by IAS, Costar, Cambridge MA
                                                                                                                                                                                                                                                  Wang, D.G., Fan, J.B., Slao, C.J., Berno, A., Young, P., Sapolsky, R., Ghandour, G., Fan, J.B., Winchester, E., Spencer, J., Kruglyak, L., Stein, L., Hale, L., Topaloglou, T., Hubbell, E., Robinson, E., Mittmann, M., Morris, M.S., Shen, N., Kilburn, D., Rioux, J., Nusbaum, C., Rozen, S., Hudson, T.J., Lipshutz, R., Chee, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172)
G43056 172 bp DNA STS 27-JAN-1999
WIAF-1517-STS Human THudson SANGER Homo sapiens STS genomic,
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Pred. No. 5.3e-56;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Thomas Hidson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research S Cambridge Center, Cambridge MA 02142 USA 9 Cambridge Center, Cambridge MA 02142 USA Fax: 617 252 1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: thudson@genome.wi.mit.edu
Primer A: TAGGCTTAAACCTGGAATCTAC
Primer B: CTCACTGGGAGGAAAAC
SIS size: 172
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Æ
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Primer: each 5 pk
dNTP8: 4 nM
Tag Polymerase: 0.5 U
Total Vol:
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Best Local Similarity 99.4%;
Matches 171; Conservative C
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                                                      sequence tagged site.
                                                                                                 GI:4191973
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Gelatin:
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27-OCT-1999 LOW-PASS SEQUENCE

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G15289/c
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Primer B: GGACGGACCAGCATCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Rimhard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STS size:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primate, Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
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STS sequence; primer; sequence tagged site.
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human STS SHGC-15950.
G15289
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67. .197
67. .88
                                                                                       complement(180.
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Total Vol:
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each 1 uM
each 200 uM
cach 200 uM
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62 degrees C
72 degrees C
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for
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Best Local Similarity 100.0%;
Matches 98; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9007 gtttttattatgaataaagaatgccatttctcacgcc 9044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8947 agottcattttatttttgacgtcactttttggccatgtaaactatttgtggcaatttat 9006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B., Colampalo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferretra, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marguis, N., McEwan, P., McGurk, A., McRernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., Oconnor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html.
NOTE: This record contains 70 individual
sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows vorelap relationships among clones to be deduced.
However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GTTTTTATTTATGAATAAAGAATGCCATTTCTCACGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (27-0CT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P_(1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTTCATTTTATTTTTGACGTCACTTTTTTGGCCATGTAAACTATTTGTGGCAATTTTAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 53967)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone 141_E_4
                                                                                                                                                                                                be preserved.
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            3792
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                                              3026
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                                            722: contig of 722 bp in length
gap of unknown length
1504: contig of 782 bp in length
2265: contig of 761 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
                                                                                                                                                                                                             is updated, the accession
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          gap of unknown length contig of 766 bp in length contig of maknown length
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of unknown length
tig of 817 bp in length
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Pred. No.
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15
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